REMARKS

By an Office Action dated April 16, 2002 in the file of this application the Examiner objected to the patent application for a variety of grounds. Based on this submission, reconsideration of the merits of this patent application is respectfully requested.

On page 2 of the Office Action, the Examiner objected to the disclosure on the grounds that it contains embedded hyperlinks. The applicant needs help with understanding this rejection. The undersigned counsel has reviewed the specification and cannot find an embedded hyperlink. If there is an embedded hyperlink in the specification, the applicant stands ready to modify the specification, but applicant's counsel cannot find the hyperlink in question. If the Examiner would care to point the applicant to this hyperlink, it will be removed.

The next rejection applied in the Office Action was a series of rejections under §112, first paragraph, beginning on page 3 of the specification. Turning to the first rejection under §112, first paragraph, the Examiner rejected a defined set of claims because the specification, while admittedly enabling for a gene encoding SEQ ID NO:2, was not enabling for other MinD genes, at least as argued by the Examiner. The applicant still believes that the Examiner is incorrectly applying the applicable standard.

First, note that the claims of this application, and in particular independent Claim 1, 14, 20 and 24 all specify two different limitations for each of the MinD genes in question. In each of those claims, it is specifically recited that the protein coding sequence encodes a protein having 80% sequence identity with the protein set forth in SEQ ID NO:2. This limitation thus specifies with exact structural specificity over 80% of the protein in question which is expressed in the transgenic plants. Furthermore, each claim has separate language which recites that the plant has altered size or shape of plasmids attributable to the genetic insert. Thus there are two criteria, a high degree of structural identity and a functional effect matching the effect demonstrated for the genetic constructs described and enabled in this patent application. Note that sequence identity is recited in the claims. The Office Action recites that the claims lack definition of hybridization or wash conditions and probes, but homology is not claimed. SEQ ID NO:2 is a protein and the claimed proteins have 80% of the identical sequence. No hybridization or wash conditions are appropriate.

In defense of the rejection, the Examiner points to the fact that the protein in question has 326 amino acids. This is true. It is also true that there are modifications to the amino acid sequence of this protein which would result in proteins which would not be effective in

changing the plastid size or number in a plant. However, plants expressing those proteins would not come within the scope of any of the claims of this patent application. It is equally true, and well within the ambit of one of ordinary skill in the art, that certain conservative amino acid substitutions can be made to virtually any protein, including those claimed here, and still preserve its functionality *in vivo*. Here the applicant has sought to both provide reasonable scope of the invention to the applicant and limit the claims to those modifications which are actually functional in plants for the defined objective. This is a reasonable interpretation of the data presented by the applicant here.

Note that the applicant has demonstrated that closely related genes having high sequence identity at the protein level to the genes described here are effective in plants and exist in other plants. The applicant found a *Tagetes* gene from just the data made available by having done work with the *Arabidopsis* gene. This demonstrates conclusively that similar genes can be found in other plants. The degree of sequence identity between the *Arabidopsis* and *Tagetes* genes was 92% (specification page 7, line 11). The applicant has stated its belief that sequences having this defined effect will be at least 80% identical at the sequence level (page 7, line 8). The applicant has thus set forth in the claims a structural limitation related to the genes at issue that is reasonable, and the claims include a function limitation which ensures that non-functional proteins will not be covered by the claims of this application. Accordingly, it is asserted by the applicant that the invention is enabled to the full breadth of the language recited in the claims of this patent application.

In any event, it is now believed that Claim 3 has been amended to be in allowable form regardless of this rejection, since it is limited by its terms to the DNA sequence set forth as SEQ ID NO:1.

On page 4 of the Office Action is another rejection to Claims 1-7 and 10-26 under §112, first paragraph, on the grounds that the antisense language is not enabled by the specification of this application. The applicant has responded herewith by removing the antisense language from Claims 1, 14, 20 and 24 and has substituted therefor a new Claim 29. Therefore this rejection will be discussed only in conjunction with the new Claim 29. The other claims should be free of this rejection.

It is asserted that Claim 29 does not suffer from the defects alleged to have been present in the earlier claims submitted by the applicant. Claim 29 recites that the sequence of the MinD gene in the target plant is known. A genetic construct is made then to lower the expression of that gene using an antisense technology. This the applicant has done, as recited in the specification, by an antisense construct directed at Arabidopsis MinD gene. Obviously,

for any given plant species, the antisense construct for that species has to be constructed for the MinD gene actually present in that plant. This is a generalized method which has been demonstrated to work in plants and which is generalizable to all plant species containing a MinD gene. It is therefore believed that this claim is not subject to the previously entered rejection in the claims related to antisense approach.

On page 6 of the Office Action is a rejection for various claims in the application under §112, first paragraph on the grounds of lack of support in the specification. The Examiner asserts that the language previously inserted in the claims was new matter. In response to this objection the applicant directs the Examiner's attention to the specification page 7, line 8 where the levels of sequence identity are set forth in the application as either 50%, or more preferably, 80%. This passage is sufficient to support the language in the claims of this application.

In the last rejection contained in the Office Action the Examiner rejected Claims 24-26 under §112, second paragraph for indefiniteness. The Examiner suggested language to the applicant which has been adopted by the applicant here. The applicant wishes to thank the Examiner for this suggestion. It is believed that this change to the claim will obviate this ground of rejection.

Wherefore the Examiner is respectfully requested to review again the merits of this patent application. A separate petition for extension of time and request for continued examination is submitted herewith so that this response can be considered as timely filed.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

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Date: October 16, 2002

Serial No.: 09/553,431

Group Art Unit: 1638

Filed: 04/19/2000

Examiner: A. Kubelik

Title: MANIPULATION OF MIN GENES IN PLANTS

File No.: 920905.90041

Please cancel Claims 9, 11-13, and amend Claims 1, 3, 6, 14, 16, 19, 20, 22, 24, and 26-28 as follows, and add the following new Claim 29:

1. (Twice Amended) A transgenic plant comprising in its genome an artificial genetic construct comprising a sense [or antisense MinD] protein coding sequence and a promoter which promotes expression of the MinD protein coding sequence in cells of the plant, wherein expression of the sequence in the plant causes alteration in the size, shape and/or number of plastids in plant cells of the plant as compared to non-transgenic plants of the species, the MinD protein encoded by the protein coding sequence having at least [a 50%] 80% sequence identity with SEQ ID NO:2.

2. The plant of Claim 1, wherein the coding sequence is selected from the group consisting of an Arabidopsis MinD protein coding sequence and a Tagetes MinD protein coding sequence.

3. (Amended) [The plant of Claim 1] A transgenic plant comprising in its genome an artificial genetic construct comprising a sense protein coding sequence and a promoter which promotes expression of the MinD protein coding sequence in cells of the plant, wherein expression of the sequence in the plant causes alteration in the size, shape and/or number of plastids in plant cells of the plant as compared to non-transgenic plants of the species, wherein the coding sequence is [selected from the group consisting of] SEQ ID NO:1[and SEQ ID NO:3].

4. The plant of Claim 1, wherein the construct comprises in 5' to 3' order a CaMV 35S promoter, a MinD protein coding sequence, and an OCS terminator.

5. The plant of Claim 4, wherein the coding sequence is selected from the group consisting of an Arabidopsis MinD protein coding sequence and a Tagetes MinD protein coding sequence.

6. (Amended) The plant of Claim 4, wherein the coding sequence is selected from the group consisting of SEQ ID NO:1 [and SEQ ID NO:3].

7. The plant of Claim 1, wherein the plastids are chloroplasts.

8. An isolated DNA sequence comprising the sequence of SEQ ID NO:1.

9. (Cancelled) A DNA sequence comprising the sequence of SEQ ID NO:3.

10. Seed of the plant of Claim 1.

11. (Cancelled) A plant comprising in its genome a transgene comprising a sense or antisense MinD gene which causes the plant to have an altered number of plastids as compared to plants of the same species without the transgene, the MinD gene encoding a protein having at least a 50% sequence identity with SEQ ID NO:2.

12. (Cancelled) Seeds of the plant of Claim 11.

13. (Cancelled) A plant as claimed in Claim 11 wherein the coding sequence of the MinD gene is selected from the group consisting of AtMinD and TeMinD.

14. (Twice Amended) A plant seed comprising in its genome a genetic construct comprising a [sense or antisense] MinD protein coding sequence and a promoter, not natively associated with the MinD protein coding sequence, which promotes expression of the MinD protein coding sequence in the plant, wherein expression of the sequence in the plant causes alteration in the size, shape and/or number of plastids in plant cells of the plant as compared to nontransgenic plants of the species, the MinD gene encoding a protein having at least [a 50%] 80% sequence identity with SEQ ID NO:2.

15. The plant of Claim 14, wherein the coding sequence is selected from the group consisting of an Arabidopsis MinD protein coding sequence and a Tagetes MinD protein coding sequence.

16. (Amended) The plant of Claim 14, wherein the coding sequence is selected from the group consisting of SEQ ID NO:1[and SEQ ID NO:3].

17. The plant of Claim 14, wherein the construct comprises in 5' to 3' order a CaMV 35S promoter, a MinD protein coding sequence, and an OCS terminator.

18. The plant of Claim 17, wherein the coding sequence is selected from the group consisting of an Arabidopsis MinD protein coding sequence and a Tagetes MinD protein coding sequence.

19. (Amended) The plant of Claim 17, wherein the coding sequence is selected from the group consisting of SEQ ID NO:1 [and SEQ ID NO:3].

20. (Twice Amended) A genetic construct comprising a MinD protein coding sequence in either a sense or antisense orientation and a promoter that promotes expression of the sequence in plants, the promoter not being natively associated with the protein coding sequence, the MinD gene encoding a protein having at least a [50%] 80% sequence identity with SEQ ID NO:2.

21. The construct of Claim 20, wherein the MinD protein coding sequence is selected from the group consisting of an Arabidopsis MinD protein coding sequence and a Tagetes MinD protein coding sequence.

22. (Amended) The construct of Claim 20, wherein the coding sequence is selected from the group consisting of SEQ ID NO:1[and SEQ ID NO:3].

23. The construct of Claim 20, wherein the promoter is a CaMV 35S promoter.

24. (Twice Amended) A method for altering the size, shape and/or number of plastids in plant cells comprising the steps of constructing a genetic construct comprising a MinD protein coding sequence [in either sense or antisense orientation] and a promoter, not natively associated with the MinD protein coding sequence, which promotes expression of the MinD protein coding sequence in plants, introducing the genetic construct into a plant, selecting a plant that has received a copy of the genetic construct, and growing the plant under conditions that allow expression of the gene, [the] thereby producing a plant [having] with altered size shape or number of plastids, the MinD gene encoding a protein having at least a [50%] 80% sequence identity with SEQ ID NO:2.

25. The method of Claim 24, wherein the coding sequence is selected from the group consisting of an Arabidopsis MinD protein coding sequence and a Tagetes MinD protein coding sequence.

26. (Amended) The method of Claim 24, wherein the coding sequence is selected from the group consisting of SEQ ID NO:1 [and SEQ ID NO:3].

27. (Twice Amended) A DNA sequence isolated from its native genome, the isolated DNA sequence comprising a plant MinD gene, the MinD gene encoding a protein having at least a [50%] 80% sequence identity with SEQ ID NO:2.

28. (Amended) The DNA sequence of Claim 27, wherein the DNA sequence is selected from the group consisting of SEQ ID NO:1 [and SEQ ID NO:3].

29. (New) A method for altering the size, shape and/or number of plastids in plant cells comprising the steps of identifying the DNA sequence of the MinD gene in that plant species, constructing a genetic construct comprising a MinD gene sequence in the antisense orientation and a promoter, not natively associated with the MinD gene sequence, which promotes transcription of the antisense MinD gene sequence in plants, introducing the genetic construct into a plant, selecting a plant that has received a copy of the genetic construct, and growing the plant under conditions that allow expression of the genetic construct, the plant having altered size shape or number of plastids.

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